

**ABSTRACT OF THE DISCLOSURE**

The invention provides a method of determining an amino acid sequence of a parent polypeptide. The method consists of: (a) obtaining mass spectra of two or more  
5 differentially labeled polypeptide fragments of a parent polypeptide; (b) assigning a mass and a weighting characteristic to two or more paired signals having a difference in mass corresponding to an integer value of said differential label, the weighting characteristic  
10 combining properties of each signal within said paired signals; (c) selecting from the mass spectra a paired signal having the assigned mass and a weighting characteristic distinguishable from non-peptide signals, the assigned mass indicating the mass of a polypeptide  
15 fragment within the spectra; (d) determining the difference in mass of the polypeptide fragments; (e) assigning the mass differences a satisfying amino acid name, and (f) orienting the assigned amino acid names. Also provided is a method of determining the amino acid  
20 sequence of a polypeptide. The method consists of: (a) constructing a graph from mass spectra of two or more differentially labeled polypeptides, the graph comprising a node with mass  $m$ , number of labels  $n$ , intensity  $i$ , and mass differential of labels  $\delta$ ; (b) creating a node  
25 corresponding to a paired signal having masses of about  $m$  and about  $m+n\delta$ , and (c) adding a labeled weighted directed edge to the graph between any two nodes corresponding to a mass of an amino acid, the labeled weighted directed edge combining properties of the paired  
30 signals.